

10/593425

H 06291/PCT

## SEQUENCE LISTING

<110> Henkel Kommanditgesellschaft auf Aktien

<120> Der Faktor RecA aus Bacillus licheniformis und recA-inaktivierte Sicherheitsstämme für die biotechnologische Produktion

<130> H 06291 PCT

<150> DE102004013988

<151> 2004-03-19

<160> 32

<170> PatentIn version 3.1

<210> 1

<211> 1047

<212> DNA

<213> Bacillus licheniformis DSM 13

<220>

<221> CDS

<222> (1)..(1047)

<223>

<220>

<221> gene

<222> (1)..(1047)

<223> recA

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1                    5                    10                    15

aag cag ttt ggt aaa ggt tcg att atg aaa ctc ggc gaa caa act gaa        96  
Lys Gln Phe Gly Lys Gly Ser Ile Met Lys Leu Gly Glu Gln Thr Glu  
20                    25                    30

acg aga att tca aca gtt ccg agc ggt tct tta gcg ctc gat gcg gct        144  
Thr Arg Ile Ser Thr Val Pro Ser Gly Ser Leu Ala Leu Asp Ala Ala  
35                    40                    45

ctt gga gtg ggc gga tac ccg cgc ggc cg att att gaa gta tac ggg        192  
Leu Gly Val Gly Gly Tyr Pro Arg Gly Arg Ile Ile Glu Val Tyr Gly  
50                    55                    60

cct gaa agc tcc ggt aaa acg acg gtg gcg ctt cat gcg att gcc gaa        240  
Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile Ala Glu  
65                    70                    75                    80

gtt cag cag cag ggc gga caa gcg gcg ttc atc gac gcc gac acc gcg        288  
Val Gln Gln Gly Gly Gln Ala Ala Phe Ile Asp Ala Asp Thr Ala  
85                    90                    95

ctt gat ccc gtc tat gca caa aag ctg ggc gtc aac att gat gag ctt        336  
Leu Asp Pro Val Tyr Ala Gln Lys Leu Gly Val Asn Ile Asp Glu Leu  
100                  105                  110

H 06291/PCT

ttg ctg tca cag cct gat acg ggc gag cag gcg ctc gaa atc gct gaa Leu Leu Ser Gln Pro Asp Thr Gly Glu Gln Ala Leu Glu Ile Ala Glu 115 120 125	384
gcc ctt gtc aga agc gga gcg gtg gat atc gtt gtc atc gac tct gta Ala Leu Val Arg Ser Gly Ala Val Asp Ile Val Val Ile Asp Ser Val 130 135 140	432
gca gcg ctt gtg ccg aaa gct gaa atc gaa gga gat atg ggg gat tcc Ala Ala Leu Val Pro Lys Ala Glu Ile Glu Gly Asp Met Gly Asp Ser 145 150 155 160	480
cac gtc ggt ttg cag gcc aga ctg atg tct cag gcg ctt cgc aag ctt His Val Gly Leu Gln Ala Arg Leu Met Ser Gln Ala Leu Arg Lys Leu 165 170 175	528
tcc gga gcg atc aat aaa tcg aag acc atc gcg atc ttt atc aac cag Ser Gly Ala Ile Asn Lys Ser Lys Thr Ile Ala Ile Phe Ile Asn Gln 180 185 190	576
att cgt gaa aaa gtc ggt gtc atg ttt gga aat cct gag acg acg cca Ile Arg Glu Lys Val Gly Val Met Phe Gly Asn Pro Glu Thr Thr Pro 195 200 205	624
ggc gga aga gcg ctg aaa ttc tac tct tct gtc cgc ctt gaa gtg cgc Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Val Arg Leu Glu Val Arg 210 215 220	672
cgc gca gag cag ctg aaa caa ggc aac gac gtc atg ggg aac aag acg Arg Ala Glu Gln Leu Lys Gln Gly Asn Asp Val Met Gly Asn Lys Thr 225 230 235 240	720
aaa atc aaa gtc gtg aaa aac aaa gtg gca cct cca ttc cgg aca gcc Lys Ile Lys Val Val Lys Asn Lys Val Ala Pro Pro Phe Arg Thr Ala 245 250 255	768
gaa gtg gac att atg tac ggg gaa gga att tca aaa gaa ggg gaa atc Glu Val Asp Ile Met Tyr Gly Glu Gly Ile Ser Lys Glu Gly Glu Ile 260 265 270	816
atc gac ctc gga aca gag ctt gac atc gtt caa aag acg ggt gca tgg Ile Asp Leu Gly Thr Glu Leu Asp Ile Val Gln Lys Ser Gly Ala Trp 275 280 285	864
tac tct tat cag gag gaa cgc ctt gga caa ggc cgt gaa aac gcc aaa Tyr Ser Tyr Gln Glu Glu Arg Leu Gly Gln Gly Arg Glu Asn Ala Lys 290 295 300	912
cag ttc ctg aaa gaa aac aag gat atc ctt ttg atg att caa gag cag Gln Phe Leu Lys Glu Asn Lys Asp Ile Leu Leu Met Ile Gln Glu Gln 305 310 315 320	960
atc cgg gag cac tac ggt ttg gat act gga ggc gct gct cct gca cag Ile Arg Glu His Tyr Gly Leu Asp Thr Gly Gly Ala Ala Pro Ala Gln 325 330 335	1008
gaa gac gag gcc caa gct cag gaa gaa ctc gag ttt taa Glu Asp Glu Ala Gln Ala Gln Glu Glu Leu Glu Phe 340 345	1047

H 06291/PCT

<210> 2  
<211> 348  
<212> PRT  
<213> *Bacillus licheniformis* DSM 13

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1 5 10 15

Lys Gln Phe Gly Lys Gly Ser Ile Met Lys Leu Gly Glu Gln Thr Glu  
20 25 30

Thr Arg Ile Ser Thr Val Pro Ser Gly Ser Leu Ala Leu Asp Ala Ala  
35 40 45

Leu Gly Val Gly Gly Tyr Pro Arg Gly Arg Ile Ile Glu Val Tyr Gly  
50 55 60

Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile Ala Glu  
65 70 75 80

Val Gln Gln Gln Gly Gly Gln Ala Ala Phe Ile Asp Ala Asp Thr Ala  
85 90 95

Leu Asp Pro Val Tyr Ala Gln Lys Leu Gly Val Asn Ile Asp Glu Leu  
100 105 110

Leu Leu Ser Gln Pro Asp Thr Gly Glu Gln Ala Leu Glu Ile Ala Glu  
115 120 125

Ala Leu Val Arg Ser Gly Ala Val Asp Ile Val Val Ile Asp Ser Val  
130 135 140

Ala Ala Leu Val Pro Lys Ala Glu Ile Glu Gly Asp Met Gly Asp Ser  
145 150 155 160

His Val Gly Leu Gln Ala Arg Leu Met Ser Gln Ala Leu Arg Lys Leu  
165 170 175

Ser Gly Ala Ile Asn Lys Ser Lys Thr Ile Ala Ile Phe Ile Asn Gln  
180 185 190

Ile Arg Glu Lys Val Gly Val Met Phe Gly Asn Pro Glu Thr Thr Pro  
195 200 205

Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Val Arg Leu Glu Val Arg

H 06291/PCT

210

215

220

Arg Ala Glu Gln Leu Lys Gln Gly Asn Asp Val Met Gly Asn Lys Thr  
225 230 235 240

Lys Ile Lys Val Val Lys Asn Lys Val Ala Pro Pro Phe Arg Thr Ala  
245 250 255

Glu Val Asp Ile Met Tyr Gly Glu Gly Ile Ser Lys Glu Gly Glu Ile  
260 265 270

Ile Asp Leu Gly Thr Glu Leu Asp Ile Val Gln Lys Ser Gly Ala Trp  
275 280 285

Tyr Ser Tyr Gln Glu Glu Arg Leu Gly Gln Gly Arg Glu Asn Ala Lys  
290 295 300

Gln Phe Leu Lys Glu Asn Lys Asp Ile Leu Leu Met Ile Gln Glu Gln  
305 310 315 320

Ile Arg Glu His Tyr Gly Leu Asp Thr Gly Gly Ala Ala Pro Ala Gln  
325 330 335

Glu Asp Glu Ala Gln Ala Gln Glu Glu Leu Glu Phe  
340 345

<210> 3

<211> 1792

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (140)..(1336)

<223>

<220>

<221> gene

<222> (1)..(1792)

<223> spoIV

<220>

<221> misc\_feature

<222> (140)..(142)

<223> First codon translated as Met.

<400> 3

ggctgatgct caaacagggg cagtgcata ttcaaggcaa agactttgtc atcaaaaacga 60

**H 06291/PCT**

ttttgcctga gaaaattctg cttgaaggca cgattgagct tgtccgctat atcgattcat	120
aagtcggggg gaaagaagc gtg aag aat aaa tgg ctt tct ttt tca gga	172
Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly	
1 5 10	
aag atc cag ctt aag ata acg gga aaa ggg atc gaa cgg tta tta aat	220
Lys Ile Gln Leu Lys Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn	
15 20 25	
gaa tgc acc agg cgc aac atc ccg atg ttt aat gta aag aaa aag aaa	268
Glu Cys Thr Arg Arg Asn Ile Pro Met Phe Asn Val Lys Lys Lys	
30 35 40	
gac gcc gtc ttt ctt tat att ccg ctt tct gat gta cat gcc ttc cgg	316
Asp Ala Val Phe Leu Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg	
45 50 55	
aag gtc atc aga ggc ttc gac tgc aag tgc agg ttc atc aaa cga aaa	364
Lys Val Ile Arg Gly Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys	
60 65 70 75	
ggg ttt cct ttc ctc gtg cag aag tct aaa cgg aat agc ggc ttc act	412
Gly Phe Pro Phe Leu Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr	
80 85 90	
ttt gga gtt gct gca ttt ttt atc atc atg ctc cta ttg tcc aac atg	460
Phe Gly Val Ala Ala Phe Phe Ile Ile Met Leu Leu Leu Ser Asn Met	
95 100 105	
ctt tgg aaa att gat att aca gga gcc aat ccg gag aca gaa cat caa	508
Leu Trp Lys Ile Asp Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln	
110 115 120	
atc aaa cag caa ttg gat caa atc ggc gtc aaa aaa ggc cgc ttt cag	556
Ile Lys Gln Gln Leu Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln	
125 130 135	
ttt tca atg ctg acc ccg gaa aaa att cag cag gcg ctc aca aag ccg	604
Phe Ser Met Leu Thr Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg	
140 145 150 155	
gtc gaa aac atc act tgg gtg ggt att gag tta aac ggc acc gcc ctt	652
Val Glu Asn Ile Thr Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu	
160 165 170	
cac atg aaa gtc gtt gaa aag aat gaa cct gac aaa gaa aaa tat atc	700
His Met Lys Val Val Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile	
175 180 185	
ggt ccg agg cac atc gtc gcc aaa aaa ggg gcg acc atc tcg aaa aag	748
Gly Pro Arg His Ile Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Lys	
190 195 200	
ttc gtg gaa aaa ggc gag ccg ctc gtc acg gtg aac cag cac gtt gaa	796
Phe Val Glu Lys Gly Glu Pro Leu Val Thr Val Asn Gln His Val Glu	
205 210 215	
aaa ggg caa atg ctc gtt tcc ggg ctg atc gga agc gaa gag gaa aag	844
Lys Gly Gln Met Leu Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys	
220 225 230 235	

H 06291/PCT

caa aaa gtc gga gca aaa ggg aaa atc tac ggt gaa acc tgg tac aag Gln Lys Val Gly Ala Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys 240 245 250	892
tca aca gta acg gtt cct ctt gag aca tca ttt gac gtt ttt acg ggt Ser Thr Val Thr Val Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly 255 260 265	940
aaa gta agg aca agt cac aag cta tcc ctc gga tca ttt tcc gtg ccg Lys Val Arg Thr Ser His Lys Leu Ser Leu Gly Ser Phe Ser Val Pro 270 275 280	988
atc tgg ggc ttt tca ttt aaa aaa gaa gac ttc tcg cgc ccg aag acg Ile Trp Gly Phe Ser Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr 285 290 295	1036
gag acc gaa aac ccc tcg ctg cat ttt atg aat ttt aag ctt cct gtc Glu Thr Glu Asn Pro Ser Leu His Phe Met Asn Phe Lys Leu Pro Val 300 305 310 315	1084
gct tat gaa aag gag cat atg agg gag agc gaa caa atc aaa agg gtg Ala Tyr Glu Lys Glu His Met Arg Glu Ser Glu Gln Ile Lys Arg Val 320 325 330	1132
tac tcg aaa aaa gaa gca gtt ctt gaa gga atc gaa atg gga aaa aga Tyr Ser Lys Lys Glu Ala Val Leu Glu Gly Ile Glu Met Gly Lys Arg 335 340 345	1180
gac atc agg aaa aaa atc ggc agc gac ggg aac att atc agt gaa aaa Asp Ile Arg Lys Lys Ile Gly Ser Asp Gly Asn Ile Ile Ser Glu Lys 350 355 360	1228
gtt ttg cac gaa acg agc gag aat ggc aaa gtt aaa ttg atc atc ctt Val Leu His Glu Thr Ser Glu Asn Gly Lys Val Lys Leu Ile Ile Leu 365 370 375	1276
tac cag gtt att gaa gac att gtt caa aca aca cca att gtt cag gag Tyr Gln Val Ile Glu Asp Ile Val Gln Thr Thr Pro Ile Val Gln Glu 380 385 390 395	1324
act aaa gaa tga cagaacactt acttgcaatt catcagcaac tggaaagtcc Thr Lys Glu	1376
 gaatgaggct caaacgctgt ttgggaacca ggattcccat ttgaagttga tggaggaaga 1436 gctgaacatt tcaatttgtca cgcgccggaga aaccgtgtat gtgacaggag atgaagaaac 1496 gtttgaaatc gcggacagcc tgcttgcctc tctcctaaat ctgatccgca aaggaatcga 1556 gatatccgaa cgcgatgtct tgtatgcgat caagatggcg aaaaagcaga agcttgagtt 1616 ttttgaaagc atgtatgaag aggaaattac gaaaaacgcc aaaggaaaac cgatcagagt 1676 caaaaccatc ggtcaaaagag aatacatcgc cgccatgaaa aggcacgact taatcttcgg 1736 catcgccccca gcaggaacgg ggaaaaaccta tttggctgtc gtaaaggccg ttcatg 1792	

**H 06291/PCT**

<211> 398

<212> PRT

<213> *Bacillus licheniformis*

<220>

<221> misc\_feature

<222> (140)..(142)

<223> First codon translated as Met.

<400> 4

Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly Lys Ile Gln Leu Lys  
1 5 10 15

Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn Glu Cys Thr Arg Arg  
20 25 30

Asn Ile Pro Met Phe Asn Val Lys Lys Lys Asp Ala Val Phe Leu  
35 40 45

Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg Lys Val Ile Arg Gly  
50 55 60

Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys Gly Phe Pro Phe Leu  
65 70 75 80

Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val Ala Ala  
85 90 95

Phe Phe Ile Ile Met Leu Leu Leu Ser Asn Met Leu Trp Lys Ile Asp  
100 105 110

Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Lys Gln Gln Leu  
115 120 125

Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met Leu Thr  
130 135 140

Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn Ile Thr  
145 150 155 160

Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys Val Val  
165 170 175

Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg His Ile  
180 185 190

Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Lys Phe Val Glu Lys Gly  
195 200 205

H 06291/PCT

Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln Met Leu  
210 215 220

Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val Gly Ala  
225 230 235 240

Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val Thr Val  
245 250 255

Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg Thr Ser  
260 265 270

His Lys Leu Ser Leu Gly Ser Phe Ser Val Pro Ile Trp Gly Phe Ser  
275 280 285

Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu Asn Pro  
290 295 300

Ser Leu His Phe Met Asn Phe Lys Leu Pro Val Ala Tyr Glu Lys Glu  
305 310 315 320

His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys Lys Glu  
325 330 335

Ala Val Leu Glu Gly Ile Glu Met Gly Lys Arg Asp Ile Arg Lys Lys  
340 345 350

Ile Gly Ser Asp Gly Asn Ile Ile Ser Glu Lys Val Leu His Glu Thr  
355 360 365

Ser Glu Asn Gly Lys Val Lys Leu Ile Ile Leu Tyr Gln Val Ile Glu  
370 375 380

Asp Ile Val Gln Thr Thr Pro Ile Val Gln Glu Thr Lys Glu  
385 390 395

<210> 5  
<211> 1594  
<212> DNA  
<213> *Bacillus subtilis*

<220>  
<221> CDS  
<222> (201)..(1397)  
<223>

**H 06291/PCT**

<220>  
<221> gene  
<222> (1)..(1594)  
<223> yqfD

<220>  
<221> misc\_feature  
<222> (201)..(203)  
<223> First codon translated as Met.

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gacttcatat ctacatagaa aaccacagag gcctttgct tttcagttag aatgaagtgc 60  
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ttcttccgga agagatactt ttggagggtt cgattgatgt cgttcgatat gttgagtcat 180  
aaagccgagg gggaaatgtt gtg aaa aat aaa tgg ctg tct ttt tcg ggt 233  
Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly  
1 5 10  
aag gtc cag ctt gaa ttg acg gga aga ggg att gag cgg ctc ctt aat 281  
Lys Val Gln Leu Glu Leu Thr Gly Arg Gly Ile Glu Arg Leu Leu Asn  
15 20 25  
gaa tgc aca aaa cag ggg att ccg gtc ttt cat gtc aaa aaa aag aaa 329  
Glu Cys Thr Lys Gln Gly Ile Pro Val Phe His Val Lys Lys Lys  
30 35 40  
gaa gcc gta tcg tta tat ata cag ctt cag gat gta cat gcc ttt cgg 377  
Glu Ala Val Ser Leu Tyr Ile Gln Leu Gln Asp Val His Ala Phe Arg  
45 50 55  
cgg gta aga agt aaa ttt aaa tgt aaa gcc cga ttt atc aat cgg aag 425  
Arg Val Arg Ser Lys Phe Lys Cys Lys Ala Arg Phe Ile Asn Arg Lys  
60 65 70 75  
gga ttt ccc ttc ctg ttg ctg aaa tca aag ctg aat ata ggg ttt acg 473  
Gly Phe Pro Phe Leu Leu Lys Ser Lys Leu Asn Ile Gly Phe Thr  
80 85 90  
atc ggt ttt gcg att ttt ttc att ctt ttg ttt ttg ctg tcc aat atg 521  
Ile Gly Phe Ala Ile Phe Phe Ile Leu Leu Phe Leu Leu Ser Asn Met  
95 100 105  
gtg tgg aaa att gat gtg aca ggc gct aag cct gaa aca gaa cat caa 569  
Val Trp Lys Ile Asp Val Thr Gly Ala Lys Pro Glu Thr Glu His Gln  
110 115 120  
atg agg cag cat ctt aat gaa atc ggc gtc aaa aag ggc cgt ctg cag 617  
Met Arg Gln His Leu Asn Glu Ile Gly Val Lys Lys Gly Arg Leu Gln  
125 130 135  
ttt tta atg atg tcg ccc gaa aaa ata cag aaa tca tta acc aat gga 665  
Phe Leu Met Met Ser Pro Glu Lys Ile Gln Lys Ser Leu Thr Asn Gly  
140 145 150 155  
ata gac aat atc act tgg gtc gga gtt gat ctg aag ggg acg acc att 713  
Ile Asp Asn Ile Thr Trp Val Gly Val Asp Leu Lys Gly Thr Thr Ile

## H 06291/PCT

	160	165	170	
cat atg aaa gtt gtg gag aaa aat gag ccc gaa aaa gaa aaa tat gtt His Met Lys Val Val Glu Lys Asn Glu Pro Glu Lys Glu Lys Tyr Val	175	180	185	761
agc ccg cgc aat att gtc gcc aaa aag aaa gca acc att acg aga atg Ser Pro Arg Asn Ile Val Ala Lys Lys Lys Ala Thr Ile Thr Arg Met	190	195	200	809
tct gtg caa aaa gga cag ccc atg gcc gcc ata cac gat cat gtt gaa Ser Val Gln Lys Gly Gln Pro Met Ala Ala Ile His Asp His Val Glu	205	210	215	857
aag gga cag ctg ctt gtt tcg gga ctg atc ggc agc gaa gac cat cag Lys Gly Gln Leu Leu Val Ser Gly Leu Ile Gly Ser Glu Asp His Gln	220	225	230	905
cag gaa gtc gcc tca aaa gca gaa att tat gga gaa acc tgg tat aga Gln Glu Val Ala Ser Lys Ala Glu Ile Tyr Gly Glu Thr Trp Tyr Arg	240	245	250	953
tca gaa gtg aca gtc ccg ctt gaa aca tta ttt aac gtc tat acg ggc Ser Glu Val Thr Val Pro Leu Glu Thr Leu Phe Asn Val Tyr Thr Gly	255	260	265	1001
aaa gta agg aca aag cac aag ctt tct ttt ggt tct ttg gca atc ccg Lys Val Arg Thr Lys His Lys Leu Ser Phe Gly Ser Leu Ala Ile Pro	270	275	280	1049
atc tgg ggg atg acg ttt aaa aaa gag gaa ttg aag cat cca aaa aca Ile Trp Gly Met Thr Phe Lys Lys Glu Glu Leu Lys His Pro Lys Thr	285	290	295	1097
gaa caa gaa aag cat tcg ctt cat ttt ctc gga ttt aag ctc cct gta Glu Gln Glu Lys His Ser Leu His Phe Leu Gly Phe Lys Leu Pro Val	300	305	310	1145
tcc tat gtc aaa gag caa acg aga gaa agt gaa gag gct ttg cga aaa Ser Tyr Val Lys Glu Gln Thr Arg Glu Ser Glu Glu Ala Leu Arg Lys	320	325	330	1193
tat aca aaa gaa gaa gca gtt caa gaa ggc att aaa ttg ggt aaa cag Tyr Thr Lys Glu Glu Ala Val Gln Glu Gly Ile Lys Leu Gly Lys Gln	335	340	345	1241
gat gta gag gat aaa ata ggc gaa aac ggc gag gtg aaa agt gaa aaa Asp Val Glu Asp Lys Ile Gly Glu Asn Gly Glu Val Lys Ser Glu Lys	350	355	360	1289
gtt ttg cac cag act gtt gag aat ggt aaa gta aag ttg att att ctc Val Leu His Gln Thr Val Glu Asn Gly Lys Val Lys Leu Ile Ile Leu	365	370	375	1337
tac caa gtt ata gaa gat atc gtt caa acc aca cct att gtc agg gag Tyr Gln Val Ile Glu Asp Ile Val Gln Thr Pro Ile Val Arg Glu	380	385	390	1385
act gaa gaa tga cagaacattt acttgcgatg aatcaaaaac tgaaaaaccc Thr Glu Glu				1437

H 06291/PCT

ggacgaggcg ct当地actct tc当地aaacca agattcttt tt当地aaattga tggagaaaaga 1497  
tctgaattta aatatacatta cgc当地ggcga gacgatttat gtttcaggcg atgatgaatc 1557  
gtt当地cagatt gc当地acaggc tgct当地ggatc gctcctc 1594

<210> 6  
<211> 398  
<212> PRT  
<213> Bacillus subtilis

<220>  
<221> misc\_feature  
<222> (201)..(203)  
<223> First codon translated as Met.

<400> 6

Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly Lys Val Gln Leu Glu  
1 5 10 15

Leu Thr Gly Arg Gly Ile Glu Arg Leu Leu Asn Glu Cys Thr Lys Gln  
20 25 30

Gly Ile Pro Val Phe His Val Lys Lys Lys Glu Ala Val Ser Leu  
35 40 45

Tyr Ile Gln Leu Gln Asp Val His Ala Phe Arg Arg Val Arg Ser Lys  
50 55 60

Phe Lys Cys Lys Ala Arg Phe Ile Asn Arg Lys Gly Phe Pro Phe Leu  
65 70 75 80

Leu Leu Lys Ser Lys Leu Asn Ile Gly Phe Thr Ile Gly Phe Ala Ile  
85 90 95

Phe Phe Ile Leu Leu Phe Leu Leu Ser Asn Met Val Trp Lys Ile Asp  
100 105 110

Val Thr Gly Ala Lys Pro Glu Thr Glu His Gln Met Arg Gln His Leu  
115 120 125

Asn Glu Ile Gly Val Lys Lys Gly Arg Leu Gln Phe Leu Met Met Ser  
130 135 140

Pro Glu Lys Ile Gln Lys Ser Leu Thr Asn Gly Ile Asp Asn Ile Thr  
145 150 155 160

Trp Val Gly Val Asp Leu Lys Gly Thr Thr Ile His Met Lys Val Val

H 06291/PCT

165	170	175
Glu Lys Asn Glu Pro Glu Lys Glu Lys Tyr Val Ser Pro Arg Asn Ile		
180	185	190
Val Ala Lys Lys Ala Thr Ile Thr Arg Met Ser Val Gln Lys Gly		
195	200	205
Gln Pro Met Ala Ala Ile His Asp His Val Glu Lys Gly Gln Leu Leu		
210	215	220
Val Ser Gly Leu Ile Gly Ser Glu Asp His Gln Gln Glu Val Ala Ser		
225	230	235
Lys Ala Glu Ile Tyr Gly Glu Thr Trp Tyr Arg Ser Glu Val Thr Val		
245	250	255
Pro Leu Glu Thr Leu Phe Asn Val Tyr Thr Gly Lys Val Arg Thr Lys		
260	265	270
His Lys Leu Ser Phe Gly Ser Leu Ala Ile Pro Ile Trp Gly Met Thr		
275	280	285
Phe Lys Lys Glu Glu Leu Lys His Pro Lys Thr Glu Gln Glu Lys His		
290	295	300
Ser Leu His Phe Leu Gly Phe Lys Leu Pro Val Ser Tyr Val Lys Glu		
305	310	315
Gln Thr Arg Glu Ser Glu Glu Ala Leu Arg Lys Tyr Thr Lys Glu Glu		
325	330	335
Ala Val Gln Glu Gly Ile Lys Leu Gly Lys Gln Asp Val Glu Asp Lys		
340	345	350
Ile Gly Glu Asn Gly Glu Val Lys Ser Glu Lys Val Leu His Gln Thr		
355	360	365
Val Glu Asn Gly Lys Val Lys Leu Ile Ile Leu Tyr Gln Val Ile Glu		
370	375	380
Asp Ile Val Gln Thr Thr Pro Ile Val Arg Glu Thr Glu Glu		
385	390	395

<210> 7  
<211> 1876

**H 06291/PCT**

<212> DNA  
<213> *Bacillus subtilis*

<220>  
<221> CDS  
<222> (201)..(1679)  
<223>

<220>  
<221> misc\_feature  
<222> (201)..(203)  
<223> First codon translated as Met.

<220>  
<221> gene  
<222> (1)..(1876)  
<223> spoIVa

<400> 7  
atgatatatgaa aaaggaatga acctttctcc cttgcataaca aataggaga aaggaaaa 60  
tatattaata gattgaggat gagaaatttt ctaaagatgt catattcaaa taggacaacg 120  
tcatacacat atagtgtcct gtgttgatt gaaagagctt aataaaattg aaaaggatag 180  
gaagtccggg aggggatcac ttg gaa aag gtc gat att ttc aag gat atc gct 233  
Leu Glu Lys Val Asp Ile Phe Lys Asp Ile Ala  
1 5 10  
gaa cga aca gga ggc gat ata tac tta gga gtc gta ggt gct gtc cgt 281  
Glu Arg Thr Gly Gly Asp Ile Tyr Leu Gly Val Val Gly Ala Val Arg  
15 20 25  
aca gga aaa tcc acg ttc att aaa aaa ttt atg gag ctt gtg gtg ctc 329  
Thr Gly Lys Ser Thr Phe Ile Lys Phe Met Glu Leu Val Val Leu  
30 35 40  
ccg aat atc agt aac gaa gca gac cgg gcc cga gcg cag gat gaa ctg 377  
Pro Asn Ile Ser Asn Glu Ala Asp Arg Ala Arg Ala Gln Asp Glu Leu  
45 50 55  
ccg cag agc gca gcc ggc aaa acc att atg act aca gag cct aaa ttt 425  
Pro Gln Ser Ala Ala Gly Lys Thr Ile Met Thr Thr Glu Pro Lys Phe  
60 65 70 75  
gtt ccg aat cag gcg atg tct gtt cat gtg tca gac gga ctc gat gtg 473  
Val Pro Asn Gln Ala Met Ser Val His Val Ser Asp Gly Leu Asp Val  
80 85 90  
aat ata aga tta gta gat tgt gta ggt tac aca gtg ccc ggc gct aaa 521  
Asn Ile Arg Leu Val Asp Cys Val Gly Tyr Thr Val Pro Gly Ala Lys  
95 100 105  
gga tat gaa gat gaa aac ggg ccg cgg atg atc aat acg cct tgg tac 569  
Gly Tyr Glu Asp Glu Asn Gly Pro Arg Met Ile Asn Thr Pro Trp Tyr  
110 115 120  
gaa gaa ccg atc cca ttt cat gag gct gct gaa atc ggc aca cga aaa 617

H 06291/PCT

Glu	Glu	Pro	Ile	Pro	Phe	His	Glu	Ala	Ala	Glu	Ile	Gly	Thr	Arg	Lys	
125							130					135				
gtc	att	caa	gaa	cac	tgc	acc	atc	gga	gtt	gtc	att	acg	aca	gac	ggc	665
Val	Ile	Gln	Glu	His	Ser	Thr	Ile	Gly	Val	Val	Ile	Thr	Thr	Asp	Gly	
140							145				150				155	
acc	att	gga	gat	atc	gcc	aga	agt	gac	tat	ata	gag	gct	gaa	gaa	aga	713
Thr	Ile	Gly	Asp	Ile	Ala	Arg	Ser	Asp	Tyr	Ile	Glu	Ala	Glu	Glu	Arg	
							160			165				170		
gtc	att	gaa	gag	ctg	aaa	gag	gtt	ggc	aaa	cct	ttt	att	atg	gtc	atc	761
Val	Ile	Glu	Glu	Leu	Lys	Glu	Val	Gly	Lys	Pro	Phe	Ile	Met	Val	Ile	
							175			180				185		
aac	tca	gtc	agg	ccg	tat	cac	ccg	gaa	acg	gaa	gcc	atg	cgc	cag	gat	809
Asn	Ser	Val	Arg	Pro	Tyr	His	Pro	Glu	Thr	Glu	Ala	Met	Arg	Gln	Asp	
							190			195				200		
tta	agc	gaa	aaa	tat	gat	atc	ccg	gta	ttg	gca	atg	agt	gta	gag	agc	857
Leu	Ser	Glu	Lys	Tyr	Asp	Ile	Pro	Val	Leu	Ala	Met	Ser	Val	Glu	Ser	
							205			210				215		
atg	cgg	gaa	tca	gat	gtg	ctg	agt	gtg	ctc	aga	gag	gcc	ctc	tac	gag	905
Met	Arg	Glu	Ser	Asp	Val	Leu	Ser	Val	Leu	Arg	Glu	Ala	Leu	Tyr	Glu	
							220			225				235		
ttt	ccg	gtg	cta	gaa	gtg	aat	gtc	aat	ctc	cca	agc	tgg	gta	atg	gtg	953
Phe	Pro	Val	Leu	Glu	Val	Asn	Val	Asn	Leu	Pro	Ser	Trp	Val	Met	Val	
							240			245				250		
ctg	aaa	gaa	aac	cat	tgg	ttg	cgt	gaa	agc	tat	cag	gag	tcc	gtg	aag	1001
Leu	Lys	Glu	Asn	His	Trp	Leu	Arg	Glu	Ser	Tyr	Gln	Glu	Ser	Val	Lys	
							255			260				265		
gaa	acg	gtt	aag	gat	att	aaa	cg	ctc	cg	gac	gta	gac	agg	gtt	gtc	1049
Glu	Thr	Val	Lys	Asp	Ile	Lys	Arg	Leu	Arg	Asp	Val	Asp	Arg	Val	Val	
							270			275				280		
ggc	caa	ttc	agc	gag	ttt	gaa	ttc	att	gaa	agt	gcc	gga	tta	gcc	gga	1097
Gly	Gln	Phe	Ser	Glu	Phe	Glu	Phe	Ile	Glu	Ser	Ala	Gly	Leu	Ala	Gly	
							285			290				295		
att	gag	ctg	g	ca	aaa	gg	gt	g	ca	g	at	gt	tt	ac	g	1145
Ile	Glu	Leu	Gly	Gln	Gly	Val	Ala	Glu	Ile	Asp	Leu	Tyr	Ala	Pro	Asp	
							300			305				310		
cat	cta	tat	gat	caa	atc	cta	aaa	gaa	gtt	gt	gg	gt	gaa	atc	aga	1193
His	Leu	Tyr	Asp	Gln	Ile	Leu	Lys	Glu	Val	Val	Gly	Val	Glu	Ile	Arg	
							320			325				330		
gga	aga	gac	cat	ctg	ctt	gag	ctc	atg	caa	gac	ttc	gcc	cat	gcg	aaa	1241
Gly	Arg	Asp	His	Leu	Leu	Glu	Leu	Met	Gln	Asp	Phe	Ala	His	Ala	Lys	
							335			340				345		
aca	gaa	tat	gat	caa	gt	tct	gat	gcc	tta	aaa	atg	gt	aaa	cag	acg	1289
Thr	Glu	Tyr	Asp	Gln	Val	Ser	Asp	Ala	Leu	Lys	Met	Val	Lys	Gln	Thr	
							350			355				360		
gga	tac	ggc	att	gca	gcg	cct	gct	tta	gct	gat	atg	agt	ctc	gat	gag	1337
Gly	Tyr	Gly	Ile	Ala	Ala	Pro	Ala	Leu	Ala	Asp	Met	Ser	Leu	Asp	Glu	

H 06291/PCT

	365	370	375	
ccg gaa att ata agg cag ggc tcg cga ttc ggt gtg agg ctg aaa gct Pro Glu Ile Ile Arg Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala	380	385	390	1385
395				
gtc gct ccg tcg atc cat atg atc aaa gta gat gtc gaa agc gaa ttc Val Ala Pro Ser Ile His Met Ile Lys Val Asp Val Glu Ser Glu Phe	400	405	410	1433
410				
gcc ccg att atc gga acg gaa aaa caa agt gaa gag ctt gta cgc tat Ala Pro Ile Ile Gly Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr	415	420	425	1481
425				
tta atg cag gac ttt gag gat gat ccg ctc tcc atc tgg aat tcc gat Leu Met Gln Asp Phe Glu Asp Asp Pro Leu Ser Ile Trp Asn Ser Asp	430	435	440	1529
440				
atc ttc gga agg tcg ctg agc tca att gtg aga gaa ggg att cag gca Ile Phe Gly Arg Ser Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala	445	450	455	1577
455				
aag ctg tca ttg atg cct gaa aac gca cg <sup>g</sup> tat aaa tta aaa gaa aca Lys Leu Ser Leu Met Pro Glu Asn Ala Arg Tyr Lys Leu Lys Glu Thr	460	465	470	1625
470				
tta gaa aga atc ata aac gaa ggc tct ggc ggc tta atc gcc atc atc Leu Glu Arg Ile Ile Asn Glu Gly Ser Gly Gly Leu Ile Ala Ile Ile	480	485	490	1673
490				
ctg taa taccggtaga cctcttata gaatggagg tctttttct ttgctcttaa Leu				1729
taatggaaaa ggatcaagga ataggatgaa aaaaggaaaa aaaggaatat tcgttcggt aatcacctta aatccttgac gagcaaggga ttgacgctt aaaatgcttg atatggcttt				1789
				1849
ttatatgtgt tactctacat acagaaa				1876
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<211> 492				
<212> PRT				
<213> Bacillus subtilis				
<220>				
<221> misc_feature				
<222> (201)..(203)				
<223> First codon translated as Met.				
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1	5	10	15	
Asp Ile Tyr Leu Gly Val Val Gly Ala Val Arg Thr Gly Lys Ser Thr				
20	25	30		

**H 06291/PCT**

Phe Ile Lys Lys Phe Met Glu Leu Val Val Leu Pro Asn Ile Ser Asn  
35 40 45

Glu Ala Asp Arg Ala Arg Ala Gln Asp Glu Leu Pro Gln Ser Ala Ala  
50 55 60

Gly Lys Thr Ile Met Thr Thr Glu Pro Lys Phe Val Pro Asn Gln Ala  
65 70 75 80

Met Ser Val His Val Ser Asp Gly Leu Asp Val Asn Ile Arg Leu Val  
85 90 95

Asp Cys Val Gly Tyr Thr Val Pro Gly Ala Lys Gly Tyr Glu Asp Glu  
100 105 110

Asn Gly Pro Arg Met Ile Asn Thr Pro Trp Tyr Glu Glu Pro Ile Pro  
115 120 125

Phe His Glu Ala Ala Glu Ile Gly Thr Arg Lys Val Ile Gln Glu His  
130 135 140

Ser Thr Ile Gly Val Val Ile Thr Thr Asp Gly Thr Ile Gly Asp Ile  
145 150 155 160

Ala Arg Ser Asp Tyr Ile Glu Ala Glu Glu Arg Val Ile Glu Glu Leu  
165 170 175

Lys Glu Val Gly Lys Pro Phe Ile Met Val Ile Asn Ser Val Arg Pro  
180 185 190

Tyr His Pro Glu Thr Glu Ala Met Arg Gln Asp Leu Ser Glu Lys Tyr  
195 200 205

Asp Ile Pro Val Leu Ala Met Ser Val Glu Ser Met Arg Glu Ser Asp  
210 215 220

Val Leu Ser Val Leu Arg Glu Ala Leu Tyr Glu Phe Pro Val Leu Glu  
225 230 235 240

Val Asn Val Asn Leu Pro Ser Trp Val Met Val Leu Lys Glu Asn His  
245 250 255

Trp Leu Arg Glu Ser Tyr Gln Glu Ser Val Lys Glu Thr Val Lys Asp  
260 265 270

Ile Lys Arg Leu Arg Asp Val Asp Arg Val Val Gly Gln Phe Ser Glu

H 06291/PCT

275

280

285

Phe Glu Phe Ile Glu Ser Ala Gly Leu Ala Gly Ile Glu Leu Gly Gln  
290 295 300

Gly Val Ala Glu Ile Asp Leu Tyr Ala Pro Asp His Leu Tyr Asp Gln  
305 310 315 320

Ile Leu Lys Glu Val Val Gly Val Glu Ile Arg Gly Arg Asp His Leu  
325 330 335

Leu Glu Leu Met Gln Asp Phe Ala His Ala Lys Thr Glu Tyr Asp Gln  
340 345 350

Val Ser Asp Ala Leu Lys Met Val Lys Gln Thr Gly Tyr Gly Ile Ala  
355 360 365

Ala Pro Ala Leu Ala Asp Met Ser Leu Asp Glu Pro Glu Ile Ile Arg  
370 375 380

Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala Val Ala Pro Ser Ile  
385 390 395 400

His Met Ile Lys Val Asp Val Glu Ser Glu Phe Ala Pro Ile Ile Gly  
405 410 415

Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr Leu Met Gln Asp Phe  
420 425 430

Glu Asp Asp Pro Leu Ser Ile Trp Asn Ser Asp Ile Phe Gly Arg Ser  
435 440 445

Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala Lys Leu Ser Leu Met  
450 455 460

Pro Glu Asn Ala Arg Tyr Lys Leu Lys Glu Thr Leu Glu Arg Ile Ile  
465 470 475 480

Asn Glu Gly Ser Gly Gly Leu Ile Ala Ile Ile Leu  
485 490

<210> 9

<211> 1675

<212> DNA

<213> Bacillus subtilis

<220>

H 06291/PCT

<221> CDS  
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<223>

<220>  
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<222> (1)..(1675)  
<223> spoIVB

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acatccattc gttcatcagt atatccaatg ttttcttca tatgacagtt ataaataagc 120  
cgtcagaagg caaaattaaa tgatgttagca gcaagtcata aagaaggtgt gggataggag 180  
cgaggagagt gaagtagtgtga atg ccc gat aac atc aga aaa gca gta ggt tta 233  
Met Pro Asp Asn Ile Arg Lys Ala Val Gly Leu  
1 5 10  
att ctc ctt gtt tcg tta tta agt gta ggt tta tgc aaa ccg cta aaa 281  
Ile Leu Val Ser Leu Leu Ser Val Gly Leu Cys Lys Pro Leu Lys  
15 20 25  
gaa tat tta ctg att cca acg caa atg aga gta ttt gaa acc caa aca 329  
Glu Tyr Leu Leu Ile Pro Thr Gln Met Arg Val Phe Glu Thr Gln Thr  
30 35 40  
caa gcg att gaa acg agt tta tcg gta aat gct cag aca tca gaa tcc 377  
Gln Ala Ile Glu Thr Ser Leu Ser Val Asn Ala Gln Thr Ser Glu Ser  
45 50 55  
tca gaa gcg ttt aca gta aag aaa gat ccg cat gaa atc aag gtg acg 425  
Ser Glu Ala Phe Thr Val Lys Lys Asp Pro His Glu Ile Lys Val Thr  
60 65 70 75  
ggc aaa aaa tca ggt gag tca gaa ttg gta tat gat ctt gcc gga ttt 473  
Gly Lys Ser Gly Glu Ser Glu Leu Val Tyr Asp Leu Ala Gly Phe  
80 85 90  
cca att aaa aaa aca aaa gtg cat gtt ctt cct gat tta aaa gtt ata 521  
Pro Ile Lys Lys Thr Lys Val His Val Leu Pro Asp Leu Lys Val Ile  
95 100 105  
cct ggc gga caa tca atc ggt gta aaa ctt cat tcc gtc ggt gtt ctt 569  
Pro Gly Gly Gln Ser Ile Gly Val Lys Leu His Ser Val Gly Val Leu  
110 115 120  
gtc gga ttt cat caa atc aat aca agt gaa ggc aaa aaa tct ccg gga 617  
Val Gly Phe His Gln Ile Asn Thr Ser Glu Gly Lys Ser Pro Gly  
125 130 135  
gaa acg gca gga att gaa gcg ggc gac atc att att gag atg aat gga 665  
Glu Thr Ala Gly Ile Glu Ala Gly Asp Ile Ile Glu Met Asn Gly  
140 145 150 155  
cag aaa att gaa aaa atg aat gat gta gcc cca ttt att caa aag gct 713  
Gln Lys Ile Glu Lys Met Asn Asp Val Ala Pro Phe Ile Gln Lys Ala  
160 165 170

H 06291/PCT

ggg aaa act ggt gaa tct tta gac tta ctg atc aaa cgt gat aaa cag Gly Lys Thr Gly Glu Ser Leu Asp Leu Leu Ile Lys Arg Asp Lys Gln 175 180 185	761
aaa atc aaa acg aag ctg atc cca gaa aag gat gaa gga gaa ggc aaa Lys Ile Lys Thr Lys Leu Ile Pro Glu Lys Asp Glu Gly Glu Gly Lys 190 195 200	809
tac aga atc ggg tta tat atc aga gat tct gct gct ggc atc ggc act Tyr Arg Ile Gly Leu Tyr Ile Arg Asp Ser Ala Ala Gly Ile Gly Thr 205 210 215	857
atg acc ttt tat gaa ccg aaa aca aaa aaa tac gga gca ctt ggc cac Met Thr Phe Tyr Glu Pro Lys Thr Lys Lys Tyr Gly Ala Leu Gly His 220 225 230 235	905
gtg att tcc gat atg gac aca aag aaa cca att gta gtg gag aat gga Val Ile Ser Asp Met Asp Thr Lys Lys Pro Ile Val Val Glu Asn Gly 240 245 250	953
gaa atc gtt aaa tcc act gta aca tca att gaa aaa ggg aca ggc ggt Glu Ile Val Lys Ser Thr Val Thr Ser Ile Glu Lys Gly Thr Gly Gly 255 260 265	1001
aat ccg gga gaa aaa ctg gcg cga ttt tcc tca gaa cgc aaa acg atc Asn Pro Gly Glu Lys Leu Ala Arg Phe Ser Ser Glu Arg Lys Thr Ile 270 275 280	1049
ggg gat att aac aga aac agc ccg ttt ggg att ttc ggc aca ctg cat Gly Asp Ile Asn Arg Asn Ser Pro Phe Gly Ile Phe Gly Thr Leu His 285 290 295	1097
cag ccg att caa aac aac ata tca gat caa gca ttg ccg gtt gcg ttt Gln Pro Ile Gln Asn Asn Ile Ser Asp Gln Ala Leu Pro Val Ala Phe 300 305 310 315	1145
tct acc gaa gtc aaa aaa ggg ccg gct gaa att tta acg gtt att gat Ser Thr Glu Val Lys Lys Gly Pro Ala Glu Ile Leu Thr Val Ile Asp 320 325 330	1193
gat gac aaa gta gaa aaa ttc gat att gaa atc gtc agc aca acg ccg Asp Asp Lys Val Glu Lys Phe Asp Ile Glu Ile Val Ser Thr Thr Pro 335 340 345	1241
caa aaa ttc cct gcg aca aaa gga atg gtg ttg aaa att acc gat cca Gln Lys Phe Pro Ala Thr Lys Gly Met Val Leu Lys Ile Thr Asp Pro 350 355 360	1289
aga ctg ttg aaa gaa aca gga ggc atc gta cag ggg atg agc gga agc Arg Leu Leu Lys Glu Thr Gly Gly Ile Val Gln Gly Met Ser Gly Ser 365 370 375	1337
ccg atc att caa aat gga aaa gtg atc ggt gct gtc acc cat gta ttt Pro Ile Ile Gln Asn Gly Lys Val Ile Gly Ala Val Thr His Val Phe 380 385 390 395	1385
gta aat gac ccg aca acg ggc tac ggt gtt cat att gaa tgg atg ctg Val Asn Asp Pro Thr Ser Gly Tyr Gly Val His Ile Glu Trp Met Leu 400 405 410	1433

H 06291/PCT

tca gaa gca gga atc gat att tat gga aaa gaa aaa gca agc tga 1478  
Ser Glu Ala Gly Ile Asp Ile Tyr Gly Lys Glu Lys Ala Ser  
415 420 425

ctgccggagt ttccggcagt ttttttattt tgatccctct tcacttctca gaatacatac 1538  
ggtaaaaatat acaaaaagaag attttcgac aaattcacgt ttccttgttt gtcaaatttc 1598  
attttagtc gaaaaacaga gaaaaacata gaataacaaa gatatgccac taatattggt 1658  
gattatgatt ttttag 1675

<210> 10  
<211> 425  
<212> PRT  
<213> Bacillus subtilis

<400> 10

Met Pro Asp Asn Ile Arg Lys Ala Val Gly Leu Ile Leu Leu Val Ser  
1 5 10 15

Leu Leu Ser Val Gly Leu Cys Lys Pro Leu Lys Glu Tyr Leu Leu Ile  
20 25 30

Pro Thr Gln Met Arg Val Phe Glu Thr Gln Thr Gln Ala Ile Glu Thr  
35 40 45

Ser Leu Ser Val Asn Ala Gln Thr Ser Glu Ser Ser Glu Ala Phe Thr  
50 55 60

Val Lys Lys Asp Pro His Glu Ile Lys Val Thr Gly Lys Lys Ser Gly  
65 70 75 80

Glu Ser Glu Leu Val Tyr Asp Leu Ala Gly Phe Pro Ile Lys Lys Thr  
85 90 95

Lys Val His Val Leu Pro Asp Leu Lys Val Ile Pro Gly Gly Gln Ser  
100 105 110

Ile Gly Val Lys Leu His Ser Val Gly Val Leu Val Gly Phe His Gln  
115 120 125

Ile Asn Thr Ser Glu Gly Lys Lys Ser Pro Gly Glu Thr Ala Gly Ile  
130 135 140

Glu Ala Gly Asp Ile Ile Glu Met Asn Gly Gln Lys Ile Glu Lys  
145 150 155 160

Met Asn Asp Val Ala Pro Phe Ile Gln Lys Ala Gly Lys Thr Gly Glu

H 06291/PCT

	165	170	175
Ser Leu Asp Leu Leu Ile Lys Arg Asp Lys Gln Lys Ile Lys Thr Lys			
180	185	190	
Leu Ile Pro Glu Lys Asp Glu Gly Glu Gly Lys Tyr Arg Ile Gly Leu			
195	200	205	
Tyr Ile Arg Asp Ser Ala Ala Gly Ile Gly Thr Met Thr Phe Tyr Glu			
210	215	220	
Pro Lys Thr Lys Lys Tyr Gly Ala Leu Gly His Val Ile Ser Asp Met			
225	230	235	240
Asp Thr Lys Lys Pro Ile Val Val Glu Asn Gly Glu Ile Val Lys Ser			
245	250	255	
Thr Val Thr Ser Ile Glu Lys Gly Thr Gly Gly Asn Pro Gly Glu Lys			
260	265	270	
Leu Ala Arg Phe Ser Ser Glu Arg Lys Thr Ile Gly Asp Ile Asn Arg			
275	280	285	
Asn Ser Pro Phe Gly Ile Phe Gly Thr Leu His Gln Pro Ile Gln Asn			
290	295	300	
Asn Ile Ser Asp Gln Ala Leu Pro Val Ala Phe Ser Thr Glu Val Lys			
305	310	315	320
Lys Gly Pro Ala Glu Ile Leu Thr Val Ile Asp Asp Asp Lys Val Glu			
325	330	335	
Lys Phe Asp Ile Glu Ile Val Ser Thr Thr Pro Gln Lys Phe Pro Ala			
340	345	350	
Thr Lys Gly Met Val Leu Lys Ile Thr Asp Pro Arg Leu Leu Lys Glu			
355	360	365	
Thr Gly Gly Ile Val Gln Gly Met Ser Gly Ser Pro Ile Ile Gln Asn			
370	375	380	
Gly Lys Val Ile Gly Ala Val Thr His Val Phe Val Asn Asp Pro Thr			
385	390	395	400
Ser Gly Tyr Gly Val His Ile Glu Trp Met Leu Ser Glu Ala Gly Ile			
405	410	415	

# H 06291/PCT

Asp Ile Tyr Gly Lys Glu Lys Ala Ser  
420 425

<210> 11  
<211> 1900  
<212> DNA  
<213> Bacillus subtilis

<220>  
<221> CDS  
<222> (201)..(1703)  
<223>

<220>  
<221> gene  
<222> (1)..(1900)  
<223> spoIVCA

<220>  
<221> misc\_feature  
<222> (201)..(203)  
<223> First codon translated as Met.

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ggacaaacag ctgttacata gcattaccca aggggtgatg catttatga aagtgataat 120  
catcgaggga ccgcaagctg acaaatgcat taacgattgc tatcattatt taataaaaact 180  
ttataggaag gagattcagg gtg ata gca ata tat gta agg gta tcg acc gag 233  
Val Ile Ala Ile Tyr Val Arg Val Ser Thr Glu  
1 5 10  
gaa caa gcg atc aag gga tcg agc atc gac agc caa atc gag gcc tgt 281  
Glu Gln Ala Ile Lys Gly Ser Ser Ile Asp Ser Gln Ile Glu Ala Cys  
15 20 25  
ata aag aaa gca ggg act aaa gat gtg ctg aag tat gca gat gaa gga 329  
Ile Lys Ala Gly Thr Lys Asp Val Leu Lys Tyr Ala Asp Glu Gly  
30 35 40  
ttt tca gga gag ctt tta gaa cgt ccg gct ttg aat cgc ttg agg gag 377  
Phe Ser Gly Glu Leu Leu Glu Arg Pro Ala Leu Asn Arg Leu Arg Glu  
45 50 55  
gat gca agc aag gga ctt ata agt caa gtc att tgt tac gat cct gac 425  
Asp Ala Ser Lys Gly Leu Ile Ser Gln Val Ile Cys Tyr Asp Pro Asp  
60 65 70 75  
cgt ctt tct cgaaaaa tta atg aat cag cta atc att gat gac gaa ttg 473  
Arg Leu Ser Arg Lys Leu Met Asn Gln Leu Ile Ile Asp Asp Glu Leu  
80 85 90  
cga aag cga aac ata cct ttg att ttt gta aat ggt gaa tac tac gcc aat 521

**H 06291/PCT**

Arg Lys Arg Asn Ile Pro Leu Ile Phe Val Asn Gly Glu Tyr Ala Asn	95	100	105	
tct cca gaa ggt caa ttg ttt ttc gca atg cgc ggg gca atc tca gaa				569
Ser Pro Glu Gly Gln Leu Phe Phe Ala Met Arg Gly Ala Ile Ser Glu				
110		115		120
ttt gaa aaa gcc aaa atc aaa gaa cgg aca tca agc ggc cga ctt caa				617
Phe Glu Lys Ala Lys Ile Lys Glu Arg Thr Ser Ser Gly Arg Leu Gln				
125		130		135
aaa atg aaa aaa ggc atg atc att aaa gat tct aaa cta tat ggc tat				665
Lys Met Lys Lys Gly Met Ile Ile Lys Asp Ser Lys Leu Tyr Gly Tyr				
140		145		150
155				
aaa ttt gtt aaa gag aaa aga act ctt gag ata tta gaa gag gaa gca				713
Lys Phe Val Lys Glu Lys Arg Thr Leu Glu Ile Leu Glu Glu Ala				
160		165		170
aaa atc att cgg atg att ttt aac tat ttc acc gat cat aaa agc cct				761
Lys Ile Ile Arg Met Ile Phe Asn Tyr Phe Thr Asp His Lys Ser Pro				
175		180		185
ttt ttc ggc aga gta aat ggt att gct cta cat tta act cag atg ggg				809
Phe Phe Gly Arg Val Asn Gly Ile Ala Leu His Leu Thr Gln Met Gly				
190		195		200
gtt aaa aca aaa aaa ggc gcc aaa gta tgg cac agg cag gtt gtt cgg				857
Val Lys Thr Lys Lys Gly Ala Lys Val Trp His Arg Gln Val Val Arg				
205		210		215
caa ata tta atg aac tct tcc tat aag ggt gaa cat aga cag tat aaa				905
Gln Ile Leu Met Asn Ser Ser Tyr Lys Gly Glu His Arg Gln Tyr Lys				
220		225		230
235				
tat gat aca gag ggt tcc tat gtt tca aag cag gca ggg aac aaa tct				953
Tyr Asp Thr Glu Gly Ser Tyr Val Ser Lys Gln Ala Gly Asn Lys Ser				
240		245		250
ata att aaa ata agg cct gaa gaa caa atc act gtg aca att cca				1001
Ile Ile Lys Ile Arg Pro Glu Glu Gln Ile Thr Val Thr Ile Pro				
255		260		265
gca att gtt cca gct gaa caa tgg gat tat gct caa gaa ctc tta ggt				1049
Ala Ile Val Pro Ala Glu Gln Trp Asp Tyr Ala Gln Glu Leu Leu Gly				
270		275		280
caa agt aaa aga aaa cac ttg agt atc agc cct cac aat tac ttg tta				1097
Gln Ser Lys Arg Lys His Leu Ser Ile Ser Pro His Asn Tyr Leu Leu				
285		290		295
tcg ggt ttg gtt aga tgc gga aaa tgc gga aat acc atg aca ggg aag				1145
Ser Gly Leu Val Arg Cys Gly Lys Cys Gly Asn Thr Met Thr Gly Lys				
300		305		310
315				
aaa aga aaa tca cat ggt aaa gac tac tat gta tat act tgc cgg aaa				1193
Lys Arg Lys Ser His Gly Lys Asp Tyr Tyr Val Tyr Thr Cys Arg Lys				
320		325		330
aat tat tct ggc gca aag gac cgc ggc tgc gga aaa gaa atg tct gag				1241
Asn Tyr Ser Gly Ala Lys Asp Arg Gly Cys Gly Lys Glu Met Ser Glu				

H 06291/PCT

	335	340	345	
aat aaa ttg aac cgg cat gta tgg ggt gaa att ttt aaa ttc atc aca Asn Lys Leu Asn Arg His Val Trp Gly Glu Ile Phe Lys Phe Ile Thr 350	355	360		1289
aat cct caa aag tat gtt tct ttt aaa gag gct gaa caa tca aat cac Asn Pro Gln Lys Tyr Val Ser Phe Lys Glu Ala Glu Gln Ser Asn His 365	370	375		1337
ctg tct gat gaa tta gaa ctt att gaa aaa gag ata gag aaa aca aaa Leu Ser Asp Glu Leu Glu Leu Ile Glu Lys Glu Ile Glu Lys Thr Lys 380	385	390		1385
aaa ggc cgc aag cgt ctt tta acg cta atc agc cta agc gat gac gat Lys Gly Arg Lys Arg Leu Leu Thr Leu Ile Ser Leu Ser Asp Asp Asp 400	405		410	1433
gat tta gac ata gat gaa atc aaa gca caa att att gaa ctg caa aaa Asp Leu Asp Ile Asp Glu Ile Lys Ala Gln Ile Ile Glu Leu Gln Lys 415	420		425	1481
aag caa aat cag ctt act gaa aag tgt aac aga atc cag tca aaa atg Lys Gln Asn Gln Leu Thr Glu Lys Cys Asn Arg Ile Gln Ser Lys Met 430	435		440	1529
aaa gtc cta gat gat acg agc tca agt gaa aat gct cta aaa aga gcc Lys Val Leu Asp Asp Thr Ser Ser Glu Asn Ala Leu Lys Arg Ala 445	450		455	1577
atc gac tat ttt caa tca atc ggt gca gat aac tta act ctt gaa gat Ile Asp Tyr Phe Gln Ser Ile Gly Ala Asp Asn Leu Thr Leu Glu Asp 460	465	470		1625
aaa aaa aca att gtt aac ttt atc gtg aaa gaa gtt acc att gtg gat Lys Lys Thr Ile Val Asn Phe Ile Val Lys Glu Val Thr Ile Val Asp 480	485		490	1673
tct gac acc ata tat att gaa acg tat taa agaggggtgt atgcacccccc Ser Asp Thr Ile Tyr Ile Glu Thr Tyr 495	500			1723
cttttgtaat tacaatctca ttttcaatac acctcgctgc atacgtcgcc acctttgtcc				1783
cttttccagc ggaatagctt tcaattcctt taataagccc gatcggtccg atggagatta				1843
agtccctctgc atcctcacct gtatttcga acttttcac aatatggcg accaagc				1900

<210> 12  
<211> 500  
<212> PRT  
<213> Bacillus subtilis

<220>  
<221> misc\_feature  
<222> (201)..(203)  
<223> First codon translated as Met.

<400> 12

**H 06291/PCT**

Val Ile Ala Ile Tyr Val Arg Val Ser Thr Glu Glu Gln Ala Ile Lys  
1 5 10 15

Gly Ser Ser Ile Asp Ser Gln Ile Glu Ala Cys Ile Lys Lys Ala Gly  
20 25 30

Thr Lys Asp Val Leu Lys Tyr Ala Asp Glu Gly Phe Ser Gly Glu Leu  
35 40 45

Leu Glu Arg Pro Ala Leu Asn Arg Leu Arg Glu Asp Ala Ser Lys Gly  
50 55 60

Leu Ile Ser Gln Val Ile Cys Tyr Asp Pro Asp Arg Leu Ser Arg Lys  
65 70 75 80

Leu Met Asn Gln Leu Ile Ile Asp Asp Glu Leu Arg Lys Arg Asn Ile  
85 90 95

Pro Leu Ile Phe Val Asn Gly Glu Tyr Ala Asn Ser Pro Glu Gly Gln  
100 105 110

Leu Phe Phe Ala Met Arg Gly Ala Ile Ser Glu Phe Glu Lys Ala Lys  
115 120 125

Ile Lys Glu Arg Thr Ser Ser Gly Arg Leu Gln Lys Met Lys Lys Gly  
130 135 140

Met Ile Ile Lys Asp Ser Lys Leu Tyr Gly Tyr Lys Phe Val Lys Glu  
145 150 155 160

Lys Arg Thr Leu Glu Ile Leu Glu Glu Ala Lys Ile Ile Arg Met  
165 170 175

Ile Phe Asn Tyr Phe Thr Asp His Lys Ser Pro Phe Phe Gly Arg Val  
180 185 190

Asn Gly Ile Ala Leu His Leu Thr Gln Met Gly Val Lys Thr Lys Lys  
195 200 205

Gly Ala Lys Val Trp His Arg Gln Val Val Arg Gln Ile Leu Met Asn  
210 215 220

Ser Ser Tyr Lys Gly Glu His Arg Gln Tyr Lys Tyr Asp Thr Glu Gly  
225 230 235 240

Ser Tyr Val Ser Lys Gln Ala Gly Asn Lys Ser Ile Ile Lys Ile Arg

H 06291/PCT

	245	250	255
Pro Glu Glu Glu Gln Ile Thr Val Thr Ile Pro Ala Ile Val Pro Ala			
260	265	270	
Glu Gln Trp Asp Tyr Ala Gln Glu Leu Leu Gly Gln Ser Lys Arg Lys			
275	280	285	
His Leu Ser Ile Ser Pro His Asn Tyr Leu Leu Ser Gly Leu Val Arg			
290	295	300	
Cys Gly Lys Cys Gly Asn Thr Met Thr Gly Lys Lys Arg Lys Ser His			
305	310	315	320
Gly Lys Asp Tyr Tyr Val Tyr Thr Cys Arg Lys Asn Tyr Ser Gly Ala			
325	330	335	
Lys Asp Arg Gly Cys Gly Lys Glu Met Ser Glu Asn Lys Leu Asn Arg			
340	345	350	
His Val Trp Gly Glu Ile Phe Lys Phe Ile Thr Asn Pro Gln Lys Tyr			
355	360	365	
Val Ser Phe Lys Glu Ala Glu Gln Ser Asn His Leu Ser Asp Glu Leu			
370	375	380	
Glu Leu Ile Glu Lys Glu Ile Glu Lys Thr Lys Lys Gly Arg Lys Arg			
385	390	395	400
Leu Leu Thr Leu Ile Ser Leu Ser Asp Asp Asp Asp Leu Asp Ile Asp			
405	410	415	
Glu Ile Lys Ala Gln Ile Ile Glu Leu Gln Lys Lys Gln Asn Gln Leu			
420	425	430	
Thr Glu Lys Cys Asn Arg Ile Gln Ser Lys Met Lys Val Leu Asp Asp			
435	440	445	
Thr Ser Ser Ser Glu Asn Ala Leu Lys Arg Ala Ile Asp Tyr Phe Gln			
450	455	460	
Ser Ile Gly Ala Asp Asn Leu Thr Leu Glu Asp Lys Lys Thr Ile Val			
465	470	475	480
Asn Phe Ile Val Lys Glu Val Thr Ile Val Asp Ser Asp Thr Ile Tyr			
485	490	495	

H 06291/PCT

Ile Glu Thr Tyr  
500

<210> 13  
<211> 868  
<212> DNA  
<213> *Bacillus subtilis*

<220>  
<221> CDS  
<222> (201)..(671)  
<223>

<220>  
<221> gene  
<222> (1)..(868)  
<223> spoIVCB

<400> 13  
ttcatccccata cctttgttca tttcaatgta tggcgcttg atgaagaata 60  
tttttaacat ttgaagtttag tatgctgctt accaaagccg gactcccccg cgagaaattt 120  
cccggtacag acacagacag cctcccggtc acatacattt acatataggc tttgcctac 180  
atacttttgt ggaggtgacg atg gtg aca ggt gtt ttc gca gcg ctc ggc ttt 233  
Met Val Thr Gly Val Phe Ala Ala Leu Gly Phe  
1 5 10  
gtt gtt aaa gag ctt gtc ttt tta gta tct tac gtg aaa aac aat gcc 281  
Val Val Lys Glu Leu Val Phe Leu Val Ser Tyr Val Lys Asn Asn Ala  
15 20 25  
ttt cca caa ccg ctc tca agc agc gaa gaa aaa aaa tac tta gag ctc 329  
Phe Pro Gln Pro Leu Ser Ser Glu Glu Lys Lys Tyr Leu Glu Leu  
30 35 40  
atg gct aaa ggg gat gaa cat gcc aga aac atg ctg att gag cat aat 377  
Met Ala Lys Gly Asp Glu His Ala Arg Asn Met Leu Ile Glu His Asn  
45 50 55  
ctt cgc ttg gtc gcc cat att gtg aaa aag ttc gaa aat aca ggt gag 425  
Leu Arg Leu Val Ala His Ile Val Lys Lys Phe Glu Asn Thr Gly Glu  
60 65 70 75  
gat gca gag gac tta atc tcc atc gga acg atc ggg ctt att aaa gga 473  
Asp Ala Glu Asp Leu Ile Ser Ile Gly Thr Ile Gly Leu Ile Lys Gly  
80 85 90  
att gaa agc tat tcc gct gga aaa ggg aca aag gtg gcg acg tat gca 521  
Ile Glu Ser Tyr Ser Ala Gly Lys Gly Thr Lys Val Ala Thr Tyr Ala  
95 100 105  
gcg agg tgt att gaa aat gag att gta att aca aaa ggg ggg tgc ata 569  
Ala Arg Cys Ile Glu Asn Glu Ile Val Ile Thr Lys Gly Gly Cys Ile  
110 115 120

H 06291/PCT

cac ccc tct tta ata cgt ttc aat ata tat ggt gtc aga atc cac aat	617
His Pro Ser Leu Ile Arg Phe Asn Ile Tyr Gly Val Arg Ile His Asn	
125 130 135	
ggt aac ttc ttt cac gat aaa gtt aac aat tgt ttt atc ttc aag	665
Gly Asn Phe Phe His Asp Lys Val Asn Asn Cys Phe Phe Ile Phe Lys	
140 145 150 155	
agt taa gttatctgca ccgattgatt gaaaatagtc gatggcttt tttagagcat	721
Ser	
tttcaattga gctcgatca tctaggactt tcattttga ctggattctg ttacacttt	781
cagtaagctg atttgcattt tttgcagtt caataatttgc tgcttgatt tcatctatgt	841
ctaaatcatc gtcatcgctt aggctga	868
<210> 14	
<211> 156	
<212> PRT	
<213> Bacillus subtilis	
<400> 14	
Met Val Thr Gly Val Phe Ala Ala Leu Gly Phe Val Val Lys Glu Leu	
1 5 10 15	
Val Phe Leu Val Ser Tyr Val Lys Asn Asn Ala Phe Pro Gln Pro Leu	
20 25 30	
Ser Ser Ser Glu Glu Lys Lys Tyr Leu Glu Leu Met Ala Lys Gly Asp	
35 40 45	
Glu His Ala Arg Asn Met Leu Ile Glu His Asn Leu Arg Leu Val Ala	
50 55 60	
His Ile Val Lys Lys Phe Glu Asn Thr Gly Glu Asp Ala Glu Asp Leu	
65 70 75 80	
Ile Ser Ile Gly Thr Ile Gly Leu Ile Lys Gly Ile Glu Ser Tyr Ser	
85 90 95	
Ala Gly Lys Gly Thr Lys Val Ala Thr Tyr Ala Ala Arg Cys Ile Glu	
100 105 110	
Asn Glu Ile Val Ile Thr Lys Gly Gly Cys Ile His Pro Ser Leu Ile	
115 120 125	
Arg Phe Asn Ile Tyr Gly Val Arg Ile His Asn Gly Asn Phe Phe His	
130 135 140	

H 06291/PCT

Asp Lys Val Asn Asn Cys Phe Phe Ile Phe Lys Ser  
145 150 155

<210> 15  
<211> 1192  
<212> DNA  
<213> *Bacillus subtilis*

<220>  
<221> CDS  
<222> (201)..(995)  
<223>

<220>  
<221> gene  
<222> (1)..(1192)  
<223> spoIVFA

<400> 15  
acaaagaat gatggctaaat attaagtcat ttttcggagt aagatcttaa tgtgatagaa 60  
tcaaagagaa gaatctgaca aagcatatgc tgtgtcaggt ttttttttgt ttttgccctgc 120  
tttggttcttg actaaaccga atatttgcca tggacaagac atatgatgta caaaccac 180  
gaatgcaaag gatgatggca atg agt cac aga gca gat gaa atc aga aaa cga 233  
Met Ser His Arg Ala Asp Glu Ile Arg Lys Arg  
1 5 10

tta gag aaa aga aga aag cag ctt tcc ggc tca aaa cgt ttc tct act 281  
Leu Glu Lys Arg Arg Lys Gln Leu Ser Gly Ser Lys Arg Phe Ser Thr  
15 20 25

cag aca gtt tct gaa aag cag aaa ccc ccg tcc tgg gtg atg gta acg 329  
Gln Thr Val Ser Glu Lys Gln Lys Pro Pro Ser Trp Val Met Val Thr  
30 35 40

gat cag gaa aag cat gga aca ctt ccg gtc tac gaa gat aac atg cca 377  
Asp Gln Glu Lys His Gly Thr Leu Pro Val Tyr Glu Asp Asn Met Pro  
45 50 55

aca ttc aac gga aaa cac cca ttg gtg aaa aca gat tca att atc ctg 425  
Thr Phe Asn Gly Lys His Pro Leu Val Lys Thr Asp Ser Ile Ile Leu  
60 65 70 75

aaa tgt ctt ctg tcg gcc tgc ctt gtt ctc gtt tca gct ata gcc tat 473  
Lys Cys Leu Leu Ser Ala Cys Leu Val Leu Val Ser Ala Ile Ala Tyr  
80 85 90

aaa aca aac att gga ccc gtc agt cag att aaa ccc gcc gta gcc aaa 521  
Lys Thr Asn Ile Gly Pro Val Ser Gln Ile Lys Pro Ala Val Ala Lys  
95 100 105

acc ttt gaa act gaa ttt caa ttt gct tca gca agc cat tgg ttc gaa 569  
Thr Phe Glu Thr Glu Phe Gln Phe Ala Ser Ala Ser His Trp Phe Glu  
110 115 120

H 06291/PCT

acc aaa ttc gga aat ccg ctt gct ttc ctg gct cct gaa cac aaa aat	617
Thr Lys Phe Gly Asn Pro Leu Ala Phe Leu Ala Pro Glu His Lys Asn	
125 130 135	
aag gaa cag cag att gaa gta ggc aaa gat ctg atc gcg cct gca tcc	665
Lys Glu Gln Gln Ile Glu Val Gly Lys Asp Leu Ile Ala Pro Ala Ser	
140 145 150 155	
ggg aaa gta cag cag gat ttt cag gac aat ggg gaa gga att aaa gtc	713
Gly Lys Val Gln Gln Asp Phe Gln Asp Asn Gly Glu Gly Ile Lys Val	
160 165 170	
gaa aca agc agt gat aag att gat agc gta aaa gaa ggc tat gtg gtt	761
Glu Thr Ser Ser Asp Lys Ile Asp Ser Val Lys Glu Gly Tyr Val Val	
175 180 185	
gaa gtc agc aaa gac agc caa acg gga ctg acg gtt aag gtg cag cat	809
Glu Val Ser Lys Asp Ser Gln Thr Gly Leu Thr Val Lys Val Gln His	
190 195 200	
gct gac aac acc tat agt atc tat ggc gag ctc aaa gat gtg gat gtt	857
Ala Asp Asn Thr Tyr Ser Ile Tyr Gly Glu Leu Lys Asp Val Asp Val	
205 210 215	
gct tta tat gat ttt gtg gat aaa ggc aaa aag ctc ggt tcg att aag	905
Ala Leu Tyr Asp Phe Val Asp Lys Gly Lys Lys Leu Gly Ser Ile Lys	
220 225 230 235	
ctt gat gat cat aat aaa ggg gtc tat tat ttt gcc atg aaa gac ggc	953
Leu Asp Asp His Asn Lys Gly Val Tyr Tyr Phe Ala Met Lys Asp Gly	
240 245 250	
gat aaa ttt att gat ccg att cag gtg att tca ttt gaa taa	995
Asp Lys Phe Ile Asp Pro Ile Gln Val Ile Ser Phe Glu	
255 260	
atggctcgac cttatcttaa agatccatgt gcatcctttt ctttgattta ttgcggcgct	1055
gggcttgctc acaggccata tgaaagcatt attatgtctg ctcctgattt tattgattca	1115
ttagactgggg catgctgctc tggctgtgtt ttttcttgg agaatcaagc gtgtttttt	1175
gctgccgttt ggcggaa	1192
<210> 16	
<211> 264	
<212> PRT	
<213> Bacillus subtilis	
<400> 16	
Met Ser His Arg Ala Asp Glu Ile Arg Lys Arg Leu Glu Lys Arg Arg	
1 5 10 15	
Lys Gln Leu Ser Gly Ser Lys Arg Phe Ser Thr Gln Thr Val Ser Glu	
20 25 30	

**H 06291/PCT**

Lys Gln Lys Pro Pro Ser Trp Val Met Val Thr Asp Gln Glu Lys His  
35 40 45

Gly Thr Leu Pro Val Tyr Glu Asp Asn Met Pro Thr Phe Asn Gly Lys  
50 55 60

His Pro Leu Val Lys Thr Asp Ser Ile Ile Leu Lys Cys Leu Leu Ser  
65 70 75 80

Ala Cys Leu Val Leu Val Ser Ala Ile Ala Tyr Lys Thr Asn Ile Gly  
85 90 95

Pro Val Ser Gln Ile Lys Pro Ala Val Ala Lys Thr Phe Glu Thr Glu  
100 105 110

Phe Gln Phe Ala Ser Ala Ser His Trp Phe Glu Thr Lys Phe Gly Asn  
115 120 125

Pro Leu Ala Phe Leu Ala Pro Glu His Lys Asn Lys Glu Gln Gln Ile  
130 135 140

Glu Val Gly Lys Asp Leu Ile Ala Pro Ala Ser Gly Lys Val Gln Gln  
145 150 155 160

Asp Phe Gln Asp Asn Gly Glu Gly Ile Lys Val Glu Thr Ser Ser Asp  
165 170 175

Lys Ile Asp Ser Val Lys Glu Gly Tyr Val Val Glu Val Ser Lys Asp  
180 185 190

Ser Gln Thr Gly Leu Thr Val Lys Val Gln His Ala Asp Asn Thr Tyr  
195 200 205

Ser Ile Tyr Gly Glu Leu Lys Asp Val Asp Val Ala Leu Tyr Asp Phe  
210 215 220

Val Asp Lys Gly Lys Lys Leu Gly Ser Ile Lys Leu Asp Asp His Asn  
225 230 235 240

Lys Gly Val Tyr Tyr Phe Ala Met Lys Asp Gly Asp Lys Phe Ile Asp  
245 250 255

Pro Ile Gln Val Ile Ser Phe Glu  
260

**H 06291/PCT**

<211> 1264  
<212> DNA  
<213> *Bacillus subtilis*

<220>  
<221> CDS  
<222> (201)..(1067)  
<223>

<220>  
<221> gene  
<222> (1)..(1264)  
<223> spoIVFB

<220>  
<221> misc\_feature  
<222> (201)..(203)  
<223> First codon translated as Met.

<400> 17  
actgacggtt aaggtgcagc atgctgacaa cacctatagt atctatggcg agctcaaaga 60  
tgtggatgtt gctttatatg attttgtgga taaaggcaaa aagctcgggtt cgattaagct 120  
tgatgatcat aataaagggg tctattatTT tgccatgaaa gacggcgata aatttattga 180  
tccgattcag gtgatttcat ttg aat aaa tgg ctc gac ctt atc tta aag atc 233  
Leu Asn Lys Trp Leu Asp Leu Ile Leu Lys Ile  
1 5 10  
cat gtg cat cct ttt ctt tgg att att gcg gcg ctg ggc ttg ctc aca 281  
His Val His Pro Phe Leu Trp Ile Ile Ala Ala Leu Gly Leu Leu Thr  
15 20 25  
ggc cat atg aaa gca tta tta tgt ctg ctc ctg att gta ttg att cat 329  
Gly His Met Lys Ala Leu Leu Cys Leu Leu Ile Val Leu Ile His  
30 35 40  
gag ctg ggg cat gct gct ctg gct gtg ttt ttt tct tgg aga atc aag 377  
Glu Leu Gly His Ala Ala Leu Ala Val Phe Phe Ser Trp Arg Ile Lys  
45 50 55  
cgt gtt ttt ttg ctg ccg ttt ggc gga acg gtc gaa gtg gaa gag cac 425  
Arg Val Phe Leu Leu Pro Phe Gly Gly Thr Val Glu Val Glu Glu His  
60 65 70 75  
ggg aat cgg ccg tta aag gaa gag ttt gcg gtc att att gcc gga cct 473  
Gly Asn Arg Pro Leu Lys Glu Glu Phe Ala Val Ile Ile Ala Gly Pro  
80 85 90  
ctt cag cac atc tgg ctt cag ttt gcc gcc tgg atg ctt gca gaa gtc 521  
Leu Gln His Ile Trp Leu Gln Phe Ala Ala Trp Met Leu Ala Glu Val  
95 100 105  
tca gtg att cat cag cat acc ttt gaa ctc ttc acc ttt tat aat ctt 569  
Ser Val Ile His Gln His Thr Phe Glu Leu Phe Thr Phe Tyr Asn Leu  
110 115 120

**H 06291/PCT**

tct atc tta ttt gtc aat tta ctg ccg atc tgg ccg ctg gat gga gga Ser Ile Leu Phe Val Asn Leu Leu Pro Ile Trp Pro Leu Asp Gly Gly	617
125 130 135	
aaa ctg tta ttt ttg ttg ttt tcc aaa cag ctg cct ttt caa aag gct Lys Leu Leu Phe Leu Leu Phe Ser Lys Gln Leu Pro Phe Gln Lys Ala	665
140 145 150 155	
cac cggtt aat cta aaa acg tcg ctc tgc ttc tgc ctg ctg ctc ggg His Arg Leu Asn Leu Lys Thr Ser Leu Cys Phe Cys Leu Leu Leu Gly	713
160 165 170	
tgc tgg gtt tta ttc gtg att cct ctg caa atc agc gca tgg gtt ttg Cys Trp Val Leu Phe Val Ile Pro Leu Gln Ile Ser Ala Trp Val Leu	761
175 180 185	
ttt gtc ttt ctg gct gtt tcc ttg ttt gag gaa tat cggtt aac agg cac Phe Val Phe Leu Ala Val Ser Leu Phe Glu Glu Tyr Arg Gln Arg His	809
190 195 200	
tat atc cat gtg aga ttt ctc ctc gaa agg tat tac gga aaa aac agg Tyr Ile His Val Arg Phe Leu Leu Glu Arg Tyr Tyr Gly Lys Asn Arg	857
205 210 215	
gag ctt gag aaa ctt ctg ccg ctg aca gta aag gcg gag gat aaa gtc Glu Leu Glu Lys Leu Leu Pro Leu Thr Val Lys Ala Glu Asp Lys Val	905
220 225 230 235	
tat cat gtg atg gcc gag ttc aaa cgt ggc tgt aag cat ccg att att Tyr His Val Met Ala Glu Phe Lys Arg Gly Cys Lys His Pro Ile Ile	953
240 245 250	
ata gaa aaa tca ggc caa aag ctc agc cag ctt gac gag aat gaa gtg Ile Glu Lys Ser Gly Gln Lys Leu Ser Gln Leu Asp Glu Asn Glu Val	1001
255 260 265	
ctg cac gct tac ttt gcc gat aag cgg acg aat tct tcc atg gag gaa Leu His Ala Tyr Phe Ala Asp Lys Arg Thr Asn Ser Ser Met Glu Glu	1049
270 275 280	
ctg ctt ctg ccc tac taa aactgattga caaacgcctt gtatTTTGGT Leu Leu Leu Pro Tyr	1097
285	
atatTTTTTA atgttatgga ttagcacca ttgctacaac cgctcagtac aggtgttaag	1157
agctttaca gccccctggatctggcgag tcttagtcta ataggaggtc cagagaatgt	1217
acgcaatcat taaaacagggc ggtaaaacaaa tcaaagttga agaaggc	1264
<210> 18	
<211> 288	
<212> PRT	
<213> <i>Bacillus subtilis</i>	
<220>	
<221> misc_feature	
<222> (201)..(203)	
<223> First codon translated as Met.	

H 06291/PCT

<400> 18

Leu Asn Lys Trp Leu Asp Leu Ile Leu Lys Ile His Val His Pro Phe  
1 5 10 15

Leu Trp Ile Ile Ala Ala Leu Gly Leu Leu Thr Gly His Met Lys Ala  
20 25 30

Leu Leu Cys Leu Leu Leu Ile Val Leu Ile His Glu Leu Gly His Ala  
35 40 45

Ala Leu Ala Val Phe Phe Ser Trp Arg Ile Lys Arg Val Phe Leu Leu  
50 55 60

Pro Phe Gly Gly Thr Val Glu Val Glu Glu His Gly Asn Arg Pro Leu  
65 70 75 80

Lys Glu Glu Phe Ala Val Ile Ile Ala Gly Pro Leu Gln His Ile Trp  
85 90 95

Leu Gln Phe Ala Ala Trp Met Leu Ala Glu Val Ser Val Ile His Gln  
100 105 110

His Thr Phe Glu Leu Phe Thr Phe Tyr Asn Leu Ser Ile Leu Phe Val  
115 120 125

Asn Leu Leu Pro Ile Trp Pro Leu Asp Gly Gly Lys Leu Leu Phe Leu  
130 135 140

Leu Phe Ser Lys Gln Leu Pro Phe Gln Lys Ala His Arg Leu Asn Leu  
145 150 155 160

Lys Thr Ser Leu Cys Phe Cys Leu Leu Leu Gly Cys Trp Val Leu Phe  
165 170 175

Val Ile Pro Leu Gln Ile Ser Ala Trp Val Leu Phe Val Phe Leu Ala  
180 185 190

Val Ser Leu Phe Glu Glu Tyr Arg Gln Arg His Tyr Ile His Val Arg  
195 200 205

Phe Leu Leu Glu Arg Tyr Tyr Gly Lys Asn Arg Glu Leu Glu Lys Leu  
210 215 220

Leu Pro Leu Thr Val Lys Ala Glu Asp Lys Val Tyr His Val Met Ala  
225 230 235 240

H 06291/PCT

Glu Phe Lys Arg Gly Cys Lys His Pro Ile Ile Ile Glu Lys Ser Gly  
245 250 255

Gln Lys Leu Ser Gln Leu Asp Glu Asn Glu Val Leu His Ala Tyr Phe  
260 265 270

Ala Asp Lys Arg Thr Asn Ser Ser Met Glu Glu Leu Leu Leu Pro Tyr  
275 280 285

<210> 19  
<211> 29  
<212> DNA  
<213> Artificial sequence

<220>  
<223> PCR-Primer spo1

<400> 19  
ggctgatgct caaacagggg cagtgcata 29

<210> 20  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR-Primer spo2

<400> 20  
catgaacggc cttaacgaca gccaa 24

<210> 21  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR-Primer spo3

<400> 21  
gtcatcaaaa cgattttgcc tgagg 25

<210> 22  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR-Primer spo4

<400> 22  
atgttctgtc ccgggattgg ctcctg 26

**H 06291/PCT**

<210> 23  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR-Primer spo6

<400> 23  
gttttgactc tgatcgaaat tctttggcg 29

<210> 24  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR-Primer spo7

<400> 24  
gcacgaaacg agcgagaatg gc 22

<210> 25  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR-Primer recA1

<400> 25  
ggaattcggc atcagcttca ctggag 26

<210> 26  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR-Primer recA2

<400> 26  
gctatgtcga ctatacccttg tttatgcgg 29

<210> 27  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR-Primer recA3

<400> 27  
gacctcgaa cagagcttga c 21

<210> 28

**H 06291/PCT**

<211> 30  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> PCR-Primer recA4  
  
<400> 28  
tcaaactgca gtcattaaga gaatggatgg

30

<210> 29  
<211> 23  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> PCR-Primer recA5  
  
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23

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26

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ttcgccggat ccaggtctgc ggtgcggaaag cggtctgcc aatacggctg ccatctgttg 180  
ctgaaaaatga tgaaaaata agcggaaacc ggatttcgg aatatcttcc tttcgaaaaaa 240

**H 06291/PCT**

ggccattcca ttttaggaga tcgattttc ctctaaaaaa aatcgaatat gcgttcgctt	300
ttttcttggc aaatccgcat aaacaaggta tagtagatat agcggaaagtg ataaaggagg	360
aaaataga atg agt gat cgt cag gca gcc tta gat atg gcg ctt aaa caa Met Ser Asp Arg Gln Ala Ala Leu Asp Met Ala Leu Lys Gln	410
1 5 10	
ata gaa aag cag ttt ggt aaa ggt tcg att atg aaa ctc ggc gaa caa Ile Glu Lys Gln Phe Gly Lys Gly Ser Ile Met Lys Leu Gly Glu Gln	458
15 20 25 30	
act gaa acg aga att tca aca gtt ccg agc ggt tct tta gcg ctc gat Thr Glu Thr Arg Ile Ser Thr Val Pro Ser Gly Ser Leu Ala Leu Asp	506
35 40 45	
gcg gct ctt gga gtg ggc gga tac ccg cgc ggc cggtt att att gaa gta Ala Ala Leu Gly Val Gly Gly Tyr Pro Arg Gly Arg Ile Ile Glu Val	554
50 55 60	
tac ggg cct gaa agc tcc ggt aaa acg acg gtg gcg ctt cat gcg att Tyr Gly Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile	602
65 70 75	
gcc gaa gtt cag cag cag ggc gga caa gcg gcg ttc atc gac gcc gaa Ala Glu Val Gln Gln Gly Gly Gln Ala Ala Phe Ile Asp Ala Glu	650
80 85 90	
cac gcg ctt gat ccc gtc tat gca caa aag ctg ggc gtc aac att gat His Ala Leu Asp Pro Val Tyr Ala Gln Lys Leu Gly Val Asn Ile Asp	698
95 100 105 110	
gag ctt ttg ctg tca cag cct gat acg ggc gag cag gcg ctc gaa atc Glu Leu Leu Ser Gln Pro Asp Thr Gly Glu Gln Ala Leu Glu Ile	746
115 120 125	
gct gaa gcc ctt gtc aga agc gga gcg gtg gat atc gtt gtc atc gac Ala Glu Ala Leu Val Arg Ser Gly Ala Val Asp Ile Val Val Ile Asp	794
130 135 140	
tct gta gca gcg ctt gtg ccg aaa gct gaa atc gaa gga gat atg ggg Ser Val Ala Ala Leu Val Pro Lys Ala Glu Ile Glu Gly Asp Met Gly	842
145 150 155	
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160 165 170	
aag ctt tcc gga gcg atc aat aaa tcg aag acc atc gcg atc ttt atc Lys Leu Ser Gly Ala Ile Asn Lys Ser Lys Thr Ile Ala Ile Phe Ile	938
175 180 185 190	
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195 200 205	
acg cca ggc gga aga gcg ctg aaa ttc tac tct tct gtc cgc ctt gaa Thr Pro Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Val Arg Leu Glu	1034
210 215 220	
gtg cgc cgc gca gag cag ctg aaa caa ggc aac gac gtc atg ggg aac	1082

**H 06291/PCT**

Val	Arg	Arg	Ala	Glu	Gln	Leu	Lys	Gln	Gly	Asn	Asp	Val	Met	Gly	Asn	
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aag	acg	aaa	atc	aaa	gtc	gtg	aaa	aac	aaa	gtg	gca	cct	cca	ttc	cg	1130
Lys	Thr	Lys	Ile	Lys	Val	Val	Lys	Asn	Lys	Val	Ala	Pro	Pro	Phe	Arg	
240					245					250						
aca	gcc	gaa	gtg	gac	att	atg	tac	ggg	gaa	gga	att	tca	aaa	gaa	ggg	1178
Thr	Ala	Glu	Val	Asp	Ile	Met	Tyr	Gly	Glu	Gly	Ile	Ser	Lys	Glu	Gly	
255					260				265				270			
gaa	atc	atc	gac	ctc	gga	aca	gag	ctt	gac	atc	gtt	caa	aag	agc	ggt	1226
Glu	Ile	Ile	Asp	Leu	Gly	Thr	Glu	Leu	Asp	Ile	Val	Gln	Lys	Ser	Gly	
275					280				285							
gca	tgg	tac	tct	tat	cag	gag	gaa	cgc	ctt	gga	caa	ggc	cgt	gaa	aac	1274
Ala	Trp	Tyr	Ser	Tyr	Gln	Glu	Glu	Arg	Leu	Gly	Gln	Gly	Arg	Glu	Asn	
290					295				300							
gcc	aaa	cag	ttc	ctg	aaa	gaa	aac	aag	gat	atc	ctt	ttg	atg	att	caa	1322
Ala	Lys	Gln	Phe	Leu	Lys	Glu	Asn	Lys	Asp	Ile	Leu	Leu	Met	Ile	Gln	
305					310				315							
gag	cag	atc	cg	gag	cac	tac	ggt	ttg	gat	act	gga	ggc	gct	gct	cct	1370
Glu	Gln	Ile	Arg	Glu	His	Tyr	Gly	Leu	Asp	Thr	Gly	Gly	Ala	Ala	Pro	
320					325				330							
gca	cag	gaa	gac	gag	gcc	caa	gct	cag	gaa	ctc	gag	ttt	taa			1415
Ala	Gln	Glu	Asp	Glu	Ala	Gln	Ala	Gln	Glu	Glu	Leu	Glu	Phe			
335					340				345							
tcatgaaacg	tgtgaaaggc	tgccggcccc	atcggcagcc	ttttacttta	ttcttcgctt											1475
tcaggcgctt	ctcttccatc	cattcttta	atgagggcag	tttgaaaggc	gtttaatcca											1535
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Lys	Gln	Phe	Gly	Lys	Gly	Ser	Ile	Met	Lys	Leu	Gly	Glu	Gln	Thr	Glu	
				20				25				30				
Thr	Arg	Ile	Ser	Thr	Val	Pro	Ser	Gly	Ser	Leu	Ala	Leu	Asp	Ala	Ala	
				35			40				45					
Leu	Gly	Val	Gly	Gly	Tyr	Pro	Arg	Gly	Arg	Ile	Ile	Glu	Val	Tyr	Gly	
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**H 06291/PCT**

Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile Ala Glu  
65 70 75 80

Val Gln Gln Gln Gly Gly Gln Ala Ala Phe Ile Asp Ala Glu His Ala  
85 90 95

Leu Asp Pro Val Tyr Ala Gln Lys Leu Gly Val Asn Ile Asp Glu Leu  
100 105 110

Leu Leu Ser Gln Pro Asp Thr Gly Glu Gln Ala Leu Glu Ile Ala Glu  
115 120 125

Ala Leu Val Arg Ser Gly Ala Val Asp Ile Val Val Ile Asp Ser Val  
130 135 140

Ala Ala Leu Val Pro Lys Ala Glu Ile Glu Gly Asp Met Gly Asp Ser  
145 150 155 160

His Val Gly Leu Gln Ala Arg Leu Met Ser Gln Ala Leu Arg Lys Leu  
165 170 175

Ser Gly Ala Ile Asn Lys Ser Lys Thr Ile Ala Ile Phe Ile Asn Gln  
180 185 190

Ile Arg Glu Lys Val Gly Val Met Phe Gly Asn Pro Glu Thr Thr Pro  
195 200 205

Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Val Arg Leu Glu Val Arg  
210 215 220

Arg Ala Glu Gln Leu Lys Gln Gly Asn Asp Val Met Gly Asn Lys Thr  
225 230 235 240

Lys Ile Lys Val Val Lys Asn Lys Val Ala Pro Pro Phe Arg Thr Ala  
245 250 255

Glu Val Asp Ile Met Tyr Gly Glu Gly Ile Ser Lys Glu Gly Glu Ile  
260 265 270

Ile Asp Leu Gly Thr Glu Leu Asp Ile Val Gln Lys Ser Gly Ala Trp  
275 280 285

Tyr Ser Tyr Gln Glu Glu Arg Leu Gly Gln Gly Arg Glu Asn Ala Lys  
290 295 300

Gln Phe Leu Lys Glu Asn Lys Asp Ile Leu Leu Met Ile Gln Glu Gln

**H 06291/PCT**

305

310

315

320

Ile Arg Glu His Tyr Gly Leu Asp Thr Gly Gly Ala Ala Pro Ala Gln  
325 330 335

Glu Asp Glu Ala Gln Ala Gln Glu Glu Leu Glu Phe  
340 345